

In the claims

Amendment to the Claims:

Please amend the claims as follows:

Please cancel claims 2 to 13, 16 to 28, 30 to 32, 34, 36 to 39, 41, 46, 47, 50, 52, 53, 55, 57, 59, 61 to 77, 80 to 83, 85, 89, 91, 95, 96, 97, 99, 100, 102 to 104, 108 to 110, 112, 114, 115, 117 to 137, 139 to 142, 144 to 148, 150 to 151, 153 to 163, 166 to 173, 176, 178 to 181, 183, 185 to 186, without prejudice.

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

Claim 1 (original): An isolated or recombinant nucleic acid comprising
a nucleic acid sequence having at least 85% sequence identity to SEQ ID
NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID
NO:3 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID
NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID
NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID
NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID
NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID
NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID
NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID
NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID
NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID
NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,
wherein the nucleic acid encodes a fluorescent polypeptide and the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection.

Claims 2 to 13 (canceled)

Claim 14 (original): The isolated or recombinant nucleic acid of claim 1, wherein the fluorescent polypeptide comprises a green fluorescent protein.

Claim 15 (original): The isolated or recombinant nucleic acid of claim 1, wherein the fluorescent polypeptide comprises a cyan fluorescent protein.

Claims 16 to 28 (canceled)

Claim 29 (original): An isolated or recombinant nucleic acid, wherein the nucleic acid comprises a sequence that hybridizes under stringent conditions to a sequence comprising

a nucleic acid sequence as set forth in SEQ ID NO:1,
a nucleic acid sequence as set forth in SEQ ID NO:3,
a nucleic acid sequence as set forth in SEQ ID NO:5,
a nucleic acid sequence as set forth in SEQ ID NO:7,
a nucleic acid sequence as set forth in SEQ ID NO:9,
a nucleic acid sequence as set forth in SEQ ID NO:11,
a nucleic acid sequence as set forth in SEQ ID NO:13,
a nucleic acid sequence as set forth in SEQ ID NO:15,
a nucleic acid sequence as set forth in SEQ ID NO:17,
a nucleic acid sequence as set forth in SEQ ID NO:19,
a nucleic acid sequence as set forth in SEQ ID NO:21,
a nucleic acid sequence as set forth in SEQ ID NO:23, or
a nucleic acid sequence as set forth in SEQ ID NO:25,
wherein the nucleic acid encodes a fluorescent polypeptide.

Claims 30 to 32 (canceled)

Claim 33 (original): A nucleic acid probe for identifying a nucleic acid encoding a fluorescent polypeptide, wherein the probe comprises at least 10 consecutive bases of a sequence comprising:

a sequence as set forth in SEQ ID NO:1,
a sequence as set forth in SEQ ID NO:3,
a sequence as set forth in SEQ ID NO:5,
a sequence as set forth in SEQ ID NO:7,
a sequence as set forth in SEQ ID NO:9,
a sequence as set forth in SEQ ID NO:11,
a sequence as set forth in SEQ ID NO:13,
a sequence as set forth in SEQ ID NO:15,
a sequence as set forth in SEQ ID NO:17,
a sequence as set forth in SEQ ID NO:19,
a sequence as set forth in SEQ ID NO:21,
a sequence as set forth in SEQ ID NO:23, or
a sequence as set forth in SEQ ID NO:25,
wherein the probe identifies the nucleic acid by binding or hybridization.

Claim 34 (canceled)

Claim 35 (original): A nucleic acid probe for identifying a nucleic acid encoding a fluorescent polypeptide, wherein the probe comprises a nucleic acid sequence comprising:

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,
a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,
a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,
a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,
a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,
a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,
a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection.

Claims 36 to 39 (canceled)

Claim 40 (original): An amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide with a fluorescent activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

Claim 41 (canceled)

Claim 42 (original): A method of amplifying a nucleic acid encoding a fluorescent polypeptide comprising amplification of a template nucleic acid with an amplification primer sequence pair capable of amplifying a nucleic acid sequence comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21,

or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof;
or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

Claim 43 (original): An expression cassette comprising a nucleic acid comprising

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof, or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

Claim 44 (original): A vector comprising a nucleic acid comprising

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

Claim 45 (original): A cloning vehicle comprising a vector as set forth in claim 44, wherein the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome.

Claims 46 to 47 (canceled)

Claim 48 (original): A transformed cell comprising a vector, wherein the vector comprises

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21,

or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof;
or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

Claim 49 (original): A transformed cell comprising

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID
NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID
NO:3 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID
NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID
NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID
NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID
NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID
NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID
NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID
NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID
NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID
NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID
NO:23 over a region of at least about 100 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID
NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence
comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

Claim 50 (canceled):

Claim 51 (original): A transgenic non-human animal comprising

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

Claims 52 and 53 (canceled)

Claim 54 (original): A transgenic plant comprising

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,
 wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,
 (ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof, or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

Claim 55 (canceled)

Claim 56 (original): A transgenic seed comprising

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,
a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,
a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,
wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,
(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof, or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

Claim 57 (canceled)

Claim 58 (original): An antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to

(i) a nucleic acid comprising
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,
a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,
a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,
a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,
 wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,
 (ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

Claim 59 (canceled)

Claim 60 (original): An isolated or recombinant polypeptide comprising
 (a) a polypeptide sequence comprising
 an amino acid sequence having at least 70% sequence identity to SEQ ID NO:2 over a region of at least about 100 residues,
 an amino acid sequence having at least 70% sequence identity to SEQ ID NO:4 over a region of at least about 100 residues,
 an amino acid sequence having at least 70% sequence identity to SEQ ID NO:6 over a region of at least about 100 residues, and
 an amino acid sequence having at least 70% sequence identity to SEQ ID NO:8 over a region of at least about 100 residues,

an amino acid sequence having at least 65% sequence identity to SEQ ID
 NO:10 over a region of at least about 100 residues,
 an amino acid sequence having at least 65% sequence identity to SEQ ID
 NO:12 over a region of at least about 100 residues,
 an amino acid sequence having at least 65% sequence identity to SEQ ID
 NO:14 over a region of at least about 100 residues,
 an amino acid sequence having at least 60% sequence identity to SEQ ID
 NO:16 over a region of at least about 100 residues,
 an amino acid sequence having at least 65% sequence identity to SEQ ID
 NO:18 over a region of at least about 100 residues,
 an amino acid sequence having at least 60% sequence identity to SEQ ID
 NO:20 over a region of at least about 100 residues,
 an amino acid sequence having at least 85% sequence identity to SEQ ID
 NO:22 over a region of at least about 100 residues,
 an amino acid sequence having at least 85% sequence identity to SEQ ID
 NO:24 over a region of at least about 100 residues,
 an amino acid sequence having at least 85% sequence identity to SEQ ID
 NO:26 over a region of at least about 100 residues,
 wherein the sequence identities are determined by analysis with a sequence
 comparison algorithm or by visual inspection; and,

(b) a polypeptide encoded by a nucleic acid comprising

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID
 NO:1 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID
 NO:3 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID
 NO:5 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 85% sequence identity to SEQ ID
 NO:7 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 75% sequence identity to SEQ ID
 NO:9 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 75% sequence identity to SEQ ID
 NO:11 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 75% sequence identity to SEQ ID
 NO:13 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 70% sequence identity to SEQ ID
 NO:15 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 75% sequence identity to SEQ ID
 NO:17 over a region of at least about 100 residues,
 a nucleic acid sequence having at least 70% sequence identity to SEQ ID
 NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or
a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,
wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,
(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof; a sequence as set forth in SEQ ID NO:17, or a subsequence thereof; a sequence as set forth in SEQ ID NO:19, or a subsequence thereof; a sequence as set forth in SEQ ID NO:21, or a subsequence thereof; a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

Claims 61 to 77 (canceled)

Claim 78 (original): A protein preparation comprising a polypeptide as set forth in claim 60, wherein the protein preparation comprises a liquid, a solid or a gel.

Claim 79 (currently amended): A homodimer or a heterodimer comprising a polypeptide of the invention as set forth in claim 60.

Claims 80 to 83 (canceled)

Claim 84 (currently amended): An immobilized fluorescent polypeptide, wherein the polypeptide comprises a sequence as set forth in claim 60 [[or claim 73]].

Claim 85 (canceled)

Claim 86 (currently amended): An array comprising an immobilized polypeptide as set forth in claim 60 [[or claim 73]].

Claim 87 (currently amended): An array comprising an immobilized nucleic acid as set forth in claim 1 [[or claim 29]].

Claim 88 (currently amended): An isolated or recombinant antibody that specifically binds to a polypeptide as set forth in claim 60 or to a polypeptide encoded by a nucleic acid as set forth in claim 1 [[or claim 29]].

Claim 89 (canceled)

Claim 90 (currently amended): A hybridoma comprising an antibody as set forth in claim [[89]] 88.

Claim 92 (original): A method of isolating or identifying a fluorescent polypeptide comprising the steps of:

- (a) providing an antibody as set forth in claim 88;
- (b) providing a sample comprising polypeptides; and
- (c) contacting the sample of step (b) with the antibody of step (a) under conditions wherein the antibody can specifically bind to the polypeptide, thereby isolating or identifying a fluorescent protein.

Claim 93 (currently amended): A method of making an anti-fluorescent protein antibody comprising administering to a non-human animal a nucleic acid as set forth in claim 1 [[or claim 29]], or a polypeptide as set forth in claim 60, in an amount sufficient to generate a humoral immune response, thereby making an anti-fluorescent protein antibody.

Claim 94 (currently amended): A method of producing a recombinant polypeptide comprising the steps of:

- (a) providing a nucleic acid operably linked to a promoter; wherein the nucleic acid comprises a sequence as set forth in claim 1 [[or claim 29]]; and
- (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide.

Claim 95 (canceled)

Claims 96 and 97 (canceled)

Claim 98 (original): A method for identifying an agent that changes a fluorescent polypeptide emission comprising the following steps:

(a) providing a polypeptide as set forth in claim 60 or a polypeptide encoded by a nucleic acid having a sequence as set forth in claim 1 or 29;

(b) providing a test agent;

(c) contacting the polypeptide of step (a) with the agent of step (b) and measuring a fluorescent activity of the polypeptide of the invention, wherein a change in the fluorescent activity measured in the presence of the test agent compared to the activity in the absence of the test agent provides a determination that the test agent changes the fluorescent activity.

Claims 99 and 100 (canceled)

Claim 101 (original): A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a sequence selected from the group consisting of a polypeptide sequence and a nucleic acid sequence, wherein the polypeptide comprises sequence as set forth in claim 60, or subsequence thereof, and the nucleic acid comprises a sequence as set forth in claim 1 or 29, or a subsequence thereof.

Claims 102 to 104 (canceled)

Claim 105 (currently amended): A computer readable medium having stored thereon a sequence selected from the group consisting of a polypeptide sequence and a nucleic acid sequence, wherein the polypeptide comprises sequence as set forth in claim 60, or subsequence thereof, and the nucleic acid comprises a sequence as set forth in claim 1 [[or claim 29]], or subsequence thereof.

Claim 106 (currently amended): A method for identifying a feature in a sequence comprising the steps of:

(a) reading the sequence using a computer program which identifies one or more features in a sequence, wherein the sequence comprises a polypeptide sequence and a nucleic acid sequence, wherein the polypeptide comprises a polypeptide sequence as set forth in claim 60, and the nucleic acid sequence comprises a sequence as set forth in claim 1 [[or claim 29]].

(b) identifying one or more features in the sequence with the computer program.

Claim 107 (currently amended): A method for comparing a first sequence to a second sequence comprising the steps of:

(a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide comprises sequence as set forth in claim 60, or subsequence thereof, and the nucleic acid comprises a sequence as set forth in claim 1 [[or claim 29]] or subsequence thereof; and

(b) determining differences between the first sequence and the second sequence with the computer program.

Claims 108 to 110 (canceled)

Claim 111 (original): A method for isolating or recovering a nucleic acid encoding a polypeptide with a fluorescent activity from an environmental sample comprising the steps of:

(a) providing an amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide with a fluorescent activity, wherein the primer pair is capable of amplifying SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ

ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 or a subsequence thereof;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and,

(c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a fluorescent polypeptide from an environmental sample.

Claim 112 (canceled)

Claim 113 (original): A method for isolating or recovering a nucleic acid encoding a polypeptide with a fluorescent activity from an environmental sample comprising the steps of:

(a) providing a polynucleotide probe comprising a sequence or a subsequence comprising:

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a);

(c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and

(d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide with a fluorescent activity from an environmental sample.

Claims 114 to 115 (canceled)

Claim 116 (original): A method of generating a variant of a nucleic acid encoding a fluorescent protein comprising the steps of:

(a) providing a template nucleic acid comprising:

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as

set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof.

Claims 117 to 137 (canceled)

Claim 138 (original): A method for modifying codons in a nucleic acid encoding a fluorescent polypeptide to increase its expression in a host cell, the method comprising

(a) providing a nucleic acid encoding a fluorescent polypeptide comprising a sequence selected from the group consisting of:

(i) a nucleic acid comprising

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:1 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:3 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:5 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:7 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:9 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:11 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:13 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:15 over a region of at least about 100 residues,

a nucleic acid sequence having at least 75% sequence identity to SEQ ID NO:17 over a region of at least about 100 residues,

a nucleic acid sequence having at least 70% sequence identity to SEQ ID NO:19 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:21 over a region of at least about 100 residues,

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:23 over a region of at least about 100 residues, or

a nucleic acid sequence having at least 85% sequence identity to SEQ ID NO:25 over a region of at least about 100 residues,

wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection; or,

(ii) a nucleic acid that hybridizes under stringent conditions to a nucleic acid comprising a sequence as set forth in SEQ ID NO:1, or a subsequence thereof; a sequence as set forth in SEQ ID NO:3, or a subsequence thereof; a sequence as set forth in SEQ ID NO:5, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:7, or a subsequence thereof; a sequence as set forth in SEQ ID NO:9, or a subsequence thereof; a sequence as set forth in SEQ ID NO:11, or a subsequence thereof; a sequence as set forth in SEQ ID NO:13, or a subsequence thereof; and, a sequence as set forth in SEQ ID NO:15, or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof, and

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid (b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

Claims 139 to 142 (canceled)

Claim 143 (original): A method for producing a library of nucleic acids encoding a plurality of modified fluorescent polypeptide active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising:

(a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence that hybridizes under stringent conditions to a sequence selected from the group consisting of a sequence as set forth in SEQ ID NO:1, a sequence as set forth in SEQ ID NO:3; a sequence as set forth in SEQ ID NO:5, a sequence as set forth in SEQ ID NO:7, a sequence as set forth in SEQ ID NO:9, a sequence as set forth in SEQ ID NO:11, a sequence as set forth in SEQ ID NO:13, and a sequence as set forth in SEQ ID NO:15 or a subsequence thereof, a sequence as set forth in SEQ ID NO:17, or a subsequence thereof, a sequence as set forth in SEQ ID NO:19, or a subsequence thereof, a sequence as set forth in SEQ ID NO:21, or a subsequence thereof, a sequence as set forth in SEQ ID NO:23, or a subsequence thereof; or, a sequence as set forth in SEQ ID NO:25, or a subsequence thereof, and the nucleic acid encodes a fluorescent polypeptide active site; and

(b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and,

(c) using the set of mutagenic oligonucleotides to generate a set of active site-encoding or substrate binding site-encoding variant nucleic acids encoding a range of amino acid variations at each amino acid codon that was mutagenized, thereby producing a library of nucleic acids encoding a plurality of modified fluorescent polypeptide active sites.

Claim 144 to 148 (canceled)

Claim 149 (currently amended): A method for determining a functional fragment of a fluorescent polypeptide comprising the steps of:

(a) providing a fluorescent polypeptide wherein the polypeptide comprises an amino acid sequence as set forth in claim 60, or, is encoded by a nucleic acid having a sequence as set forth in claim 1 [[or claim 29]]; and

(b) deleting a plurality of amino acid residues from the sequence of step (a) and testing the remaining subsequence for a fluorescent activity, thereby determining a functional fragment of a fluorescent polypeptide.

Claims 150 to 151 (canceled)

Claim 152 (currently amended): A method for producing a chimeric polypeptide comprising the following steps:

- (a) providing a fluorescent polypeptide wherein the polypeptide comprises an amino acid sequence as set forth in claim 60, or, is encoded by a nucleic acid having a sequence as set forth in claim 1 [[or claim 29]]; and
- (b) providing a second polypeptide; and
- (c) contacting the polypeptide of step (a) and the second polypeptide of step (b) under conditions wherein the fluorescent polypeptide can be fused with the second polypeptide, thereby producing a chimeric polypeptide.

Claims 153 to 163 (canceled)

Claim 164 (currently amended): A method for producing a nucleic acid with a fluorescent tag comprising of following steps:

- (a) providing a first fluorescent polypeptide wherein the polypeptide comprises an amino acid sequence as set forth in claim 60, or, is encoded by a nucleic acid having a sequence as set forth in claim 1 [[or claim 29]]; and
- (b) providing a nucleic acid; and
- (c) contacting the polypeptide of step (a) and the nucleic acid of step (b) under conditions wherein the fluorescent polypeptide can covalently bind with the nucleic acid, thereby producing a nucleic acid with a fluorescent tag.

Claim 165 (currently amended): A method for using a polypeptide as a fluorescent marker comprising the following steps:

- (a) providing a fluorescent polypeptide wherein the polypeptide comprises an amino acid sequence as set forth in claim 60, or, is encoded by a nucleic acid having a sequence as set forth in claim 1 [[or claim 29]]; or a chimeric polypeptide of claim 153, or a chimeric compound of claim 161, or a nucleic acid with a fluorescent tag of claim 164;
- (b) providing an excitation source emitting light at the absorption wavelength of the fluorescent polypeptide; and

(c) detecting a fluorescent activity of the compound of step (a) at the emission wavelength of the fluorescent polypeptide.

Claims 166 to 173 (canceled)

Claim 174 (original): A method for using a fluorescent polypeptide in gene therapy comprising the following steps:

- (a) obtaining from a patient a viable sample of primary cells of a particular cell type;
 - (b) inserting in the cells of step (a) a nucleic acid segment encoding a desired gene product;
 - (c) introducing in the cell of step (b) a vector comprising a nucleic acid of the invention;
 - (d) identifying and isolating cells or cell lines that express the gene product of step (b);
 - (e) re-introducing the cells that express the gene product;
 - (f) removing from the patient an aliquot of tissue including cells resulting from step (d) and their progeny;
 - (g) determining the quantity of the cells resulting from the step (d) in the aliquot of step (f),
- thereby the introduction of the vector comprising the nucleic acid of the invention in addition to the desired gene allows the identification of viable cells that contain and express the desired gene of step b.

Claim 175 (original): A method of gene therapy comprising the following steps:

- (a) providing a plurality of tissue cells;
- (b) providing a retroviral vector encoding a desired gene product;
- (c) providing a vector of the invention; and
- (d) contacting the target cells of step (a) with the retroviral vectors of step (b) and a vector of the invention under conditions wherein the cells of step (a) are transfected with the vectors of steps (b) and (c) allowing co-expression of the polypeptide of the invention, thereby allowing assessment of proportion of transfected cells and levels of expression.

Claim 176 (canceled)

Claim 177 (original): A method for diagnostic testing comprising the following steps:

- (a) providing a vector of the invention as set forth in claim 44;
- (b) placing the vector of step (a) under control of a promoter;
- (c) providing an inducing agent to induce the promoter of step (b); and
- (d) contacting the agent of step (c) with the promoter of step (b) under condition wherein the agent of step (c) induces the promoter of step (b), thereby causing the expression of a fluorescent polypeptide in cells, cell lines or tissues, wherein the cells, cell lines or tissue will become fluorescent in the presence of the inducing agent.

Claims 178 to 181 (canceled)

Claim 182 (currently amended): A method for assessing the effect of selected culture components and conditions on selected gene expression comprising the following steps:

- (a) providing a cell comprising a nucleic acid as set forth in claim 1 [[or claim 29]] operably linked to a regulatory sequence derived from a selected gene;
- (b) incubating the cell of step (a) under selected culture conditions or in the presence of selected components, wherein expressing the polypeptide of the invention; and
- (c) detecting the presence and subcellular localization of fluorescent signal thereby assessing the effect of selected cultures components or condition on selected gene expression.

Claim 183 (canceled)

Claim 184 (currently amended): A method for assessing a mutagenic potential of a test agent in a tissue culture or transgenic animal comprising the following steps:

- (a) providing the nucleic acid of the invention as set forth in claim 1 [[or claim 29]] operably linked to a transcriptional control element, wherein the transcription control element can be negatively regulated by a repressor;
- (b) providing a repressor under control of a constitutively expressed gene;

(c) providing a test compound capable of interacting with a promoter of the constitutively expressed gene thereby turning it off; and

(d) contacting the test agent of step (c) with the repressor of step (b) under conditions wherein the test agent inactivates or turns off the gene expressing the repressor thereby causing the expression of the polypeptide of the invention.

Claims 185 to 186 (canceled)

Claim 187 (currently amended): A method for identifying a compound capable of changing expression of a target gene comprising of the following steps:

(a) providing a first nucleic acid having a sequence as set forth in claim 1 [[or claim 29]] and expressing a first polypeptide, wherein the nucleic acid is operably linked to a promoter of a target gene in a cell;

(b) providing a second nucleic acid as set forth in claim 1 or 29, and expressing a second polypeptide, wherein the second nucleic acid is operably linked to a promoter of a constitutively expressed gene in a cell, wherein the first polypeptide emits a light at a wavelength different than the wavelength of the light emitted by the second polypeptide;

(c) providing a compound affecting the expression of the target gene of step (a) by binding to the promoter of the target gene;

(d) contacting the compound of step (c) with the cell of step (a);

(e) expressing the first and second polypeptide, and

(f) detecting fluorescence of the first and second polypeptides,

(i) wherein altered fluorescence of the first polypeptide and unchanged fluorescence of the second polypeptide demonstrates that the compound binds to the target gene promoter and has no non-specific or cytotoxic effects thereby not altering expression of the second polypeptide; or

(ii) wherein altered fluorescence of the first polypeptide and altered fluorescence of the second polypeptide demonstrates that the test drug has non-specific or cytotoxic effects thereby affecting the expression of the second polypeptide.

Claim 188 (original): An isolated or recombinant nucleic acid comprising a sequence having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%,

76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197.

Claim 189 (original): An isolated or recombinant nucleic acid comprising a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID

NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197.

Claim 190 (original): An isolated or recombinant polypeptide comprising a sequence having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; SEQ ID NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198.

Claim 191 (original): An isolated or recombinant polypeptide having a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198.

Claim 192 (original): An isolated or recombinant nucleic acid having a sequence comprising any combination of segments whose overhangs as described in Figure 15 can anneal to each other.